

GerCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:15 ; Search time 63.43 Seconds
 (without alignments)
 679.107 Million cell updates/sec

Title: US-09-502-984B-37
 Perfect score: 1284
 Sequence: 1 KFESKAALLAARGPEELLCF RKNERLEEVERLQLVLGER 249

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTRREMBL_19:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriapl:*

17: sp_archeapl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	903.5	70.4	509	6 Q9NYZ9	Q9NYZ9 sus scrofa
2	888	69.2	316	11 Q35545	Q35545 rattus norvegicus
3	782	60.9	229	6 Q27950	Q27950 bos indicus
4	778	60.6	229	6 Q28206	Q28206 bos taurus
5	719.5	56.0	387	6 Q95N13	Q95N13 ovis aries
6	719.5	56.0	418	6 Q95N14	Q95N14 ovis aries
7	152	11.8	566	11 Q925F5	Q925F5 mus musculus
8	133.5	10.4	422	4 Q75462	Q75462 homo sapiens
9	132.5	10.3	422	4 Q9UHHS	Q9UHHS homo sapiens
10	128.5	10.0	425	11 Q9JM58	Q9JM58 mus musculus
11	118	9.2	296	6 Q18880	Q18880 bos taurus
12	114.5	8.9	521	4 Q96TF0	Q96TF0 homo sapiens
13	112.5	8.8	581	6 Q46561	Q46561 ovis aries
14	112.5	8.8	634	6 Q46600	Q46600 bos taurus
15	111.5	8.7	626	13 Q90WG7	Q90WG7 cynops pyrus
16	108	8.4	353	3 Q96UT3	Q96UT3 saccharomyces cerevisiae

ALIGNMENTS

RESULT ID	Q9NYZ9	PRELIMINARY;	PRT;	509 AA.
Q9NYZ9	Q9NYZ9;	PRELIMINARY;	PRT;	509 AA.
AC	Q9NYZ9;			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	ERYTHROPOIETIN RECEPTOR.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,			
RA	Christenson R.K., Vallet J.L.,			
RT	"Porcine Erythropoietin Receptor: Molecular Cloning and Expression in Embryonic and Fetal Liver."			
RT	Domest. Anim. Endocrinol. 0:0-0(2000).			
RL	DR EMBL: AF274305; AAF77065.1; -.			
DR	DR HSSP; P19235; 1 EBA.			
DR	DR Interpro; IPR002996; CRLA.			
DR	DR Interpro; IPR00572; Euk_oxidore_molyb.			
DR	DR Interpro; IPR03961; FN_III.			
DR	DR Interpro; IPR03528; Hematopo_receptor_L1_F1.			
DR	DR Pfam; PF00041; fn3; 1.			
DR	DR SMART; SM00060; FN3; 1.			
DR	DR PROSITE; PS01353; HEMATOPO_REC_L1_F1; UNKNOWN_1.			
DR	DR PROSITE; PS00559; MOLYBDOPERTIN_EUK; UNKNOWN_1.			
DR	DR Receptor.			
SQ	SEQUENCE: 509 AA; 55183 MW; 35B565D07C6BCD8A CRC64;			
Query Match	70.4%; Score 903.5; DB 6; Length 509;			
Best Local Similarity	80.2%; Pred. No. 2.5e-71;			
Matches	170; Conservative 18; Mismatches 23; Indels 1; Gaps 1;			
OY	1 KFESKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSQLEDEPWKLCLRL 60			

DR	InterPro; IPR02996; C1A.	123	ENRAGGAQREVEILDGRTCECLSNLNGGTRYTMARMAPSFEGFWASWEPASLLT
DR	InterPro; IPR03528; Hematopo_receptor_L_FL.		
DR	Pfam; PF00041; fn3_1.		
DR	SMART; SM00060; FN3_1.		
DR	PROSITE; PS01352; HEMATopo_REC_L_FL; UNKNOWN_1.		
KW	Receptor.		
FT	NON_TER 1		
FT	NON_TER 229 AA; 229 MW; EDFAA6FL10D992E8 CRC64;		
SQ	SEQUENCE		
Query Match	60.6%; Score 778; DB 6; Length 229;		
Best Local Similarity	78.5%; Pred. No. 1e-60;		
Matches	146; Conservative 14; Mismatches 26; Indels 0; Gaps 0;		
RESULT	5		
Q95N13	PRELIMINARY; PRT; 387 AA.		
AC	Q95N13;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	ERYTHROPOETIN RECEPTOR (FRAGMENT).		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Caprinae; Ovis.		
OC	NCBI_TaxID:9940;		
RN	[1]		
SEQUENCE FROM N.A.			
Q95N13	"Quantitation of the mRNA levels of Epo and EpoR in various tissues in the ovine fetus".		
Q95N13	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
Db	61 PLELHVTAAAGSASRHRTHVNEVVLIDPPARLVARRADEGGHVVLRLWLPAGMASL1 120		
QY	146 RFELDI SAGINAGAGSIVORVELLIEGRTECLSVLSNLRGGTRYTIVARMAEAPSFGFWASWSE 205		
Db	121 RYEVNISAENAGSAQRVETLDRTECLLSNLRGGRTRYTFMVRARMAEAPSFGFWASWSE 180		
QY	206 PVSLLT 211		
Db	181 PASLLT 186		
RESULT	5		
Q95N13	PRELIMINARY; PRT; 387 AA.		
AC	Q95N13;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	ERYTHROPOETIN RECEPTOR (FRAGMENT).		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.		
OC	NCBI_TaxID:9940;		
RN	[1]		
SEQUENCE FROM N.A.			
RA	David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;		
RP	"Quantitation of the mRNA levels of Epo and EpoR in various tissues in the ovine fetus"; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
RA	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
RA	EMBL: AY029232; AAK38737.1; -.		
RE	Receptor.		
FT	NON_TER 1		
FT	NON_TER 387 AA; 42039 MW; 0D1E6173C432EBC6 CRC64;		
SQ	SEQUENCE		
Query Match	56.0%; Score 719.5; DB 6; Length 387;		
Best Local Similarity	76.4%; Pred. No. 2.8e-55;		
Matches	136; Conservative 14; Mismatches 27; Indels 1; Gaps 1;		
RESULT	7		
Q925F5	PRELIMINARY; PRT; 566 AA.		
ID	Q925F5		
AC	Q925F5;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	C-MPL-II		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TaxID:10090;		
RN	[1]		
SEQUENCE FROM N.A.			
RA	Sabath D.F., Lofton-Day C., Lin N., Lok S., Kaushansky K.,		
RA	Broudy V.C.;		
RT	"Identification and characterization of an isoform of murine Mpl".		
RT	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AB360122; AAK52492.1; -.		
SQ	SEQUENCE 566 AA; 63339 MW; A19D3DD5FF7BDBA6B CRC64;		
Query Match	11.8%; Score 152; DB 11; Length 566;		
Best Local Similarity	24.9%; Pred. No. 4.1e-05;		
Matches	55; Conservative 28; Mismatches 96; Indels 42; Gaps 8;		
QY	4 SKAANILAAKGPEELICLFTERLEDCVCFEREAASAGVGPONFSFSIQLDEPWKLCLRLHQA 63		
QY	95 -SGAHRFRHVTINNEVLLAFLPGVLLARLADEGHRYVTRWLPPPEPMTSHRFELDISA 153		
Db	63 SSGASRYRRTTHVNEVVLDPARLVARRADEGGHVVLRLPPGAPMASL1RYEVNISA 122		
Db	3 ATAGYGPDNFSFSYQLEGEPKWPKCRLHOTPTARGLYVRFWCSLPTADTSFVPLELHVTA 62		
QY	154 GNGAGGSIVORVELLIEGRTECLSVLSNLRGGTRYTIVARMAEAPSFGFWASWEPASLLT 211		
Db	123 ENAAGGAQREVEILDGRTCECLLSNLRGGRTRYTFMVRARMAEAPSFGFWASWEPASLLT 180		

Db	18	SDQDFVFLALGTEELFELNCFSQTFEDLTFCWDEERA-PSGTQQLYAYRGERPACPLYSQ	75	Db	296	CRLAGLPGPTVVFQVQCN---PFGIYGSKKAGIWESEWHTAATPRSERPGPGGAC	351
Qy	64	PTARGAIRFWCISLPTA-TSSEVPLERLTAAS-GAPRFHRVHII-----NE	108	Qy	219	EKLEQKVRELLRNERLEEVER-LKQLVG	247
Db	76	SVPTEFGTRYVCOFPQADEVRLFPLHVKVNUVSNQTLIQRTFVNSVETCPTLMNPNP	135	Db	352	EP-----RGEPSSGPVRELKOFGLG	372
Qy	109	VVLLDARAVGLVARLADEGHVVIRWLPPETPMTHIRFELDISAGNGAGSVORVELLEG	168	Qy	136	VPFLDQPCVHFTASQ-PHGTVTSEAGEAF-----LWKGSS-----	173
Db	169	RTECVLISNLRGRTRITAVRARMMAEPSFGGFWSSAWSEPVSL	209	Qy	174	--CLVSGLQAGKSYWQLRSOPDGVLRLGSNGPWSFPVTV	211
RESULT	8			RESULT	9		
ID	075462	PRELIMINARY;	PRT;	ID	090H5	PRELIMINARY;	PRT;
AC	075462;		422 AA.	AC	09UH5		422 AA.
DT	01-NOV-1998 (TREMBrel. 08, Created)			DT	01-MAY-2000 (TREMBrel. 13, Created)		
DT	01-NOV-1998 (TREMBrel. 08, Last sequence update)			DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)		
DE	CYTOKINE-LIKE FACTOR-1 PRECURSOR.			DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)		
GN	CIF-1.			DE	CLASS I CYTOKINE RECEPTOR.		
OS	Homo sapiens (Human).			GN	ZCYT05.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OS	Homo sapiens (Human).		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	NCBI_TaxID:9606;			OX	NCBI_TaxID:9606;		
RN	{1}			RN	{1}		
RP	SEQUENCE FROM N.A.			RP	SEQUENCE FROM N.A.		
RA	Lok S., Presnell S. R., Jelberg A. C., Gilbert T., Whitmore T. E.,			RA	Foster D. C., Adams R. L., Lehner J. M., O'Hara P. J.;		
RA	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.			RA	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.		
RL	EMBL; AF059493; AAC28335.1; -.			RL	EMBL; AF178844; AAD54385.1; -.		
DR	EMBL; AF073515; AAD39681.1; -.			DR	EMBL; AF178844; AAD54385.1; -.		
DR	HSSP; P16471; 1B33.			DR	HSSP; P16471; 1B33.		
DR	InterPro; IPR002996; CRLA.			DR	InterPro; IPR002996; CRLA.		
DR	InterPro; IPR003961; FN_III.			DR	InterPro; IPR003961; FN_III.		
DR	pfam; PF00041; fn3; 2.			DR	pfam; PF00041; fn3; 2.		
DR	SMART; SM00660; FN3; 2.			DR	SMART; SM00660; FN3; 2.		
RN	[2]			RN	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.			RP	SEQUENCE FROM N.A.		
RA	Magrangeas F., Jacques Y., Minvielle S.;			RA	Magrangeas F., Jacques Y., Minvielle S.;		
RT	'Cloning and expression of a novel soluble protein containing hematopoietic cytokine receptor domains.'			RT	'Cloning and expression of a novel soluble protein containing hematopoietic cytokine receptor domains.'		
RL	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.			RL	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF059493; AAC28335.1; -.			DR	EMBL; AF073515; AAD39681.1; -.		
DR	HSSP; P16471; 1B33.			DR	HSSP; P16471; 1B33.		
DR	InterPro; IPR002996; CRLA.			DR	InterPro; IPR002996; CRLA.		
DR	InterPro; IPR003961; FN_III.			DR	InterPro; IPR003961; FN_III.		
DR	pfam; PF00041; fn3; 2.			DR	pfam; PF00041; fn3; 2.		
DR	SMART; SM00660; FN3; 2.			DR	SMART; SM00660; FN3; 2.		
FT	SIGNAL	1		FT	SIGNAL	1	
FT	POTENTIAL.			FT	POTENTIAL.		
SEQUENCE	422 AA;	46301 MW;	AD9DEFCCB1B84228 CRC64;	SEQUENCE	422 AA;	46315 MW;	0D2C5F7A01B942EE CRC64;
Query Match				Query Match			
Best Local Similarity	10.4%	Score	133.5;	Best Local Similarity	10.3%	Score	132.5;
Best Local Similarity	23.7%	DB	4;	Best Local Similarity	23.7%	DB	4;
Matches	64;	Pred.	No. 0.0012;	Matches	64;	Pred.	No. 0.0015;
Matches	Conservative			Matches	Conservative		
Matches	37;	Mismatches	37;	Matches	37;	Mismatches	98;
Matches	Mismatches			Matches	Mismatches		
Matches	98;	Indels	71;	Matches	98;	Indels	71;
Matches	Gaps			Matches	Gaps		
Matches	16;	Length	422;	Matches	16;	Length	422;
Qy	14	PEELCCTERLEDLWVFFEEAASAGVPG-----NFSFSQLEDEPW---KLCRL	60	Qy	14	PEELCCTERLEDLWVFFEEAASAGVPG-----NFSFSQLEDEPW---KLCRL	60
Db	138	PVNISCKSNKMKDLTCRWT-----PGAGGETFLHTNYSKVKUR--WYQGDNTECE	186	Db	138	PVNISCKSNKMKDLTCRWT-----PGAGGETFLHTNYSKVKUR--WYQGDNTECE	186
Qy	61	HOAPTARGAIRFWCISLPTA-TSSEVPLERLTAAS-GAPRFHRVHII-----NE	117	Qy	61	HOAPTARGAIRFWCISLPTA-TSSEVPLERLTAAS-GAPRFHRVHII-----NE	117
Db	187	YHTVGPHS---CHIP-KDLALFTPEIWEATNRGSAKSVDLTDILDVTTDPPE	240	Db	187	YHTVGPHS---CHIP-KDLALFTPEIWEATNRGSAKSVDLTDILDVTTDPPE	240
Qy	118	L-VARLADEGHVVIRWLPPET-----PMTHIRFELDISAGNGAGSVORVELLEG	171	Qy	118	L-VARLADEGHVVIRWLPPET-----PMTHIRFELDISAGNGAGSVORVELLEG	171
Db	241	VHRSVYGGLEDOLSVRNVSPAKLDFLQAOQYQIRYRVEDSV-----DWKVVDVSNQTS	295	Db	241	VHRSVYGGLEDOLSVRNVSPAKLDFLQAOQYQIRYRVEDSV-----DWKVVDVSNQTS	295
Qy	172	CVLSNLRGRTRITAVRARMMAEPSFG-----PFGIYGSKKAGIWESEWHTAATPR	218	Qy	172	CVLSNLRGRTRITAVRARMMAEPSFG-----PFGIYGSKKAGIWESEWHTAATPR	218
Db	296	CRLAGLPGPTVVFQVQCN---PFGIYGSKKAGIWESEWHTAATPRSERPGPGGAC	351	Db	296	CRLAGLPGPTVVFQVQCN---PFGIYGSKKAGIWESEWHTAATPRSERPGPGGAC	351
Qy	219	EKLEQKVRELLRNERLEEVER-LKQLVG	247	Qy	219	EKLEQKVRELLRNERLEEVER-LKQLVG	247
Db	352	EP-----RGEPSSGPVRELKOFGLG	372	Db	352	EP-----RGEPSSGPVRELKOFGLG	372
Qy	173	Q9JMS8	PRELIMINARY;	Qy	173	Q9JMS8	PRELIMINARY;
AC	Q9JMS8;			AC	Q9JMS8;		
DT	01-DEC-2000 (TREMBrel. 15, Created)			DT	01-DEC-2000 (TREMBrel. 15, Last sequence update)		
DT	01-OCT-2000 (TREMBrel. 15, Last annotation update)			DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)		
DE	CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.			DE	CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.		
GN	CRFL1 OR CRML3.			GN	CRFL1 OR CRML3.		
OS	Mus musculus (Mouse).			OS	Mus musculus (Mouse).		
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.			OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.		
OC	NCBI_TaxID:10090;			OC	NCBI_TaxID:10090;		

RA	SEQUENCE FROM N.A.	9.2%; Score 118; DB 6; Length 296;
RA	Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.,	Best Local Similarity 21.9%; Pred. No. 0.018;
RT	"cytokine receptor like molecule 3."	Matches 48; Conservative 40; Mismatches 101; Indels 30; Gaps 10;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
DR	HSSP; P16471; IBP3.	7 ALLAARGPER----LICFTERLEDVCFEEAASAGVPGNFSFSFOLEDEPKWICRLHQ 62
DR	MGD; MGT; 1340030; Crlf1.	8 : : : : : : : : : : : : : : : : :
DR	InterPro; IPR020296; CRLA.	95 ---CILRESECTVWLPEAVLVPDSNFTTIPHRMGRQVSLSVLPDVEPLRRAVKLDR 150
DR	PFAM; PF00041; FN3; 2.	QY 116 VGLVARLADESGHVVIRWLPPTMHSIRFELDISAGNGA-GSVQVELLEGRTECV 173
DR	SMART; SM00060; FN3; 1.	Db 151* SDLOSSIS--SGHCLTWSISPALEMPTTLYSEAFKKOEEAWQAOHRDHIVQVTLI 208
KW	Signal; Receptor.	QY 174 LSNL-----RGTRITAVRAR--MAAPSFSGFWSAWSEPVY- 208
FT	SIGNAL 1	Db 209 LEAFFLDPGFIHEARLVRVOMATLEDDVVEERYTQWSEWSQVPCFOAQPORGPLIPWNG 268
SQ	SEQUENCE 425 AA; 34 POTENTIAL SIGNALS; MW: 910535C629CA7056 CRC64;	QY 209 -----LLGGGGSRMEKEQVKELLRN 232
Query Match 8.9%; Score 114.5; DB 4; Length 521;		
Best Local Similarity 22.1%; Pred. No. 0.074; Matches 61; Conservative 32; Mismatches 110; Indels 73; Gaps 12;		
Matches 61; Conservative 32; Mismatches 110; Indels 73; Gaps 12;		
QY	PERLICFTERLEDVCFEEAASAGVPGNFSFSFOLEDEPKWICRLHQ 60	QY 7 ALLAARGPER----LICFTERLEDVCFEEAASAGVPGNFSFSFOLEDEPKWICRLHQ 62
Db	141 PENISCSNRNMKDLCRMT-----PGAHGETFLHTNPLSNSYKLR--WYQDQNTICE 189	Db 8 : : : : : : : : : : : : : : : : :
QY	61 HOAPTARGAIRFWCSLPTADTSFVPLERLRTAS- GAPPFH-RVTHINEVLLDAPW 117	Db 9 : : : : : : : : : : : : : : : : :
Db	190 VHTVGVPHS----CHIP-KDLAGFLPTPEIIVWEATNRUGSARSVDTLVDVWTTDPPEPD 243	Db 10 : : : : : : : : : : : : : : : : :
QY	118 L-VARLADESGHVVIRWLPPTMHSIRFELDISAGNGA-GSVQVELLEGRTECV 171	Db 11 : : : : : : : : : : : : : : : : :
Db	244 VHVSRYVGLEDQLSVWVSPPAIKDFLEQAKYQIRYRVEDSV---DWKVWDDVSNOTS 298	Db 12 : : : : : : : : : : : : : : : : :
QY	172 CYLSNLNRGRTITAVRARRMASBPSFG-----GFWSSAWSERPVLTLT---GGGSRM 218	Db 13 : : : : : : : : : : : : : : : : :
Db	299 CRLAGLAKPTGVFVQVRNC-----PFGIGSKKAGIWSWWSHSPAASTPRSERPGGGCV 354	Db 14 : : : : : : : : : : : : : : : : :
QY	219 ERLEQVKELLRKNERLEEVEVER-LKQWLG 247	Db 15 : : : : : : : : : : : : : : : : :
Db	355 EP-----RGEPSSGPVVRRELKQFLG 375	Db 16 : : : : : : : : : : : : : : : : :
RESULT 11		
OS	018800 PRELIMINARY; PRT; 296 AA.	RESULT 12
ID	018800 PRELIMINARY; PRT; 296 AA.	ID 096TFO
AC	018800; 01880; (TREMBLEL; 05, Created)	AC 096TFO
DT	01-JAN-1998 (TREMBLEL; 05, Last sequence update)	DT 01-DEC-2001 (TREMBLEL; 19, last annotation update)
DE	INTERLEUKIN 9 RECEPTOR.	DE INTERLEUKIN 9 RECEPTOR.
GN		GN IL9R.
OS		OS Homo sapiens (Human).
OC		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA		RA Ciccodicola A., D'Esposito M., Esposito T., Gianfrancesco F.,
RA		RA Migliaccio C., Miano M.G., Matarazzo M.R., Vacca M., Franze A.,
RA		RA Cuccirese M., Coccia M., Cuccia A., Terracciano A., Torino A.,
RA		RA Coccia S., Mercadante G., Pandone E., Archidiacono N., Rocchi M.,
RA		RA Schlessinger D., D'Urso M.,
RT		RT "Differentially regulated and evolved genes in the fully sequenced
RT		RT Xq/Yq pseudoautosomal region;"
RL		RL Hum. Mol. Genet. 9:3395-401(2000).
DR		DR EMBL: AJ271736; CAB96817.1; -.
KW		KW Receptor.
SQ	SEQUENCE 521 AA; 57146 MW; 07E40436466173F3 CRC64;	SQ
Query Match 8.9%; Score 114.5; DB 4; Length 521;		
Best Local Similarity 22.1%; Pred. No. 0.074; Matches 61; Conservative 32; Mismatches 110; Indels 73; Gaps 12;		
Matches 61; Conservative 32; Mismatches 110; Indels 73; Gaps 12;		
QY	SEQUENCE FROM N.A.	QY 12 RGPEE--LICFTERLEDVCFEEAASAGVPGNFSFSFOLEDEPKWICRLHQ 69
RP	SEQUENCE FROM N.A.	Db 47 QGPRSRFTCILNNITRIDCHW-SAPEL3G-----SSPWLFTSNQAPGGTHK 94
RX	MEDLINE=9735450; PubMed=9231767;	QY 70 IRFWCSLPTADTSFVPLERLRTAAG-APRFHRVHINE-----VLLDAP 115
RA	Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;	Db 95 ---CILRESECTVWLPEAVLVPDSNFTTIPHRMGRQVSLSVLPDVEPLRRAVKLDR 150
RT	"Prolactin receptor heterogeneity in bovine fetal and maternal	QY 116 VGLVARLADESGHVVIRWLPPTMHSIRFELDISAGNGA-GSVQVELLEGRTECV 173
RT	tissues;"	Db 151* SDLOSSIS--SGHCLTWSISPALEMPTTLYSEAFKKOEEAWQAOHRDHIVQVTLI 208
RL	Endocrinology 138:3187-3194(1997).	QY 174 LSNL-----RGTRITAVRAR--MAAPSFSGFWSAWSEPVY- 208
DR	EMBL; AF027403; AAB83999.1; -.	Db 209 LEAFFLDPGFIHEARLVRVOMATLEDDVVEERYTQWSEWSQVPCFOAQPORGPLIPWNG 268
DR	HSSP; P14787; IAN3.	QY 209 -----LLGGGGSRMEKEQVKELLRN 232
DR	InterPro; IPR020296; CRLA.	
DR	InterPro; IPR03961; FN3; 2.	
DR	InterPro; IPR0328; Hematopo_receptor_L_F1.	
DR	Pfam; PF00041; FN3; 2.	
DR	SMART; SM00060; FN3; 2.	
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.	
KW	Receptor.	
SQ	SEQUENCE 296 AA; 33854 MW; 9F1C15FB41E0787 CRC64;	

Db	269 WPGNTLVAVSIFLLTGPVYLLFKLSPRVKRIFYQ 304
RESULT	13
ID	046561 PRELIMINARY; PRT; 581 AA.
AC	Q46561; P79205; O46573; P79203; O46569;
DT	01-JUN-1998 (TREMBREL. 06, Last sequence update)
DR	01-JUN-2001 (TREMBREL. 17, Last annotation update)
DE	PROLACTIN RECEPTOR PRECURSOR (PRL-R) (OPR).
OS	Ovis aries (Sheep); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
OX	NCBI_TAXID=9940;
RN	[1]
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC	TISSUE=MAMMARY GLAND, AND LIVER;
RX	Medline=98001468; PubMed=3443303;
RA	Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;
RT	"Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents.";
RL	J. Mol. Endocrinol. 19:109-120(1997).
RN	[2]
RP	SEQUENCE OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING.
RC	STRAIN=SCOTTISH BLACKFACE / ISOLATE M2280; TISSUE=ANTERIOR PITUITARY;
RX	Medline=99049302; PubMed=363452;
RA	Tortonese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;
RT	"Detection of prolactin receptor gene expression in the sheep pituitary gland and visualization of the specific translation of the signal in gonadotropins.";
RT	Endocrinology 139:5215-5223(1998).
RN	[3]
RP	SEQUENCE OF 147-302 FROM N.A., AND ALTERNATIVE SPLICING.
RC	TISSUE=FETAL LIVER, AND CORPUS LUTEUM;
RA	Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;
RT	"Two forms of the prolactin receptor messenger ribonucleic acid are present in ovine fetal liver and adult ovary.";
RL	Endocrine 3:291-295(1995).
CC	-1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- ALTERNATIVE PRODUCTS: THREE ISOFORMS; LONG ISOFORM (L-OPR) (SHOWN HERE), SHORT ISOFORM (S-OPR) AND SOLUBLE ISOFORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (LIVER, PITUITARY, ADRENAL GLAND, OVARY AND FETAL LIVER).
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. CONTAINS A FIBRONECTIN TYPE III-LIKE DOMAINS.
DR	EMBL; AF041257; AAB96920.1; -.
DR	EMBL; AF041977; AAB96920.1; -.
DR	EMBL; AF041979; AAB97082.1; -.
DR	EMBL; AF042358; AAB97744.1; -.
DR	EMBL; AF042358; AAB97743.1; -.
DR	EMBL; AF041978; AAB9595.1; -.
DR	EMBL; V10578; CAN71597.1; -.
DR	EMBL; V10808; CAN71766.1; -.
DR	HSSP; P14787; 1A3.
DR	InterPro; IPR002956; CRLA.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR003528; Hematopo_receptor_L_F1.
DR	Pfam; PF00041; Fn3; 2.
DR	SMART; SM00606; FN3; 2.
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW	Receptor; Transmembrane; Glycoprotein; Signal; Repeat; Alternative splicing.
FT	SIGNAL 1 POTENTIAL.
FT	PROLACTIN RECEPTOR.
FT	DOMAIN 25 581 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 238 258 POTENTIAL.
FT	DOMAIN 259 581 CITOPLASMIC (POTENTIAL).
RESULT	14
ID	046600 PRELIMINARY; PRT; 634 AA.
AC	O46600; P79205; O46573; P79203; O46569;
DT	01-JUN-1998 (TREMBREL. 06, Last sequence update)
DR	01-DEC-2001 (TREMBREL. 19, Last annotation update)
DE	SOMATOTROPIN RECEPTOR 1B PRECURSOR.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Bos.
OX	NCBI_TAXID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=HOLSTEIN;
RA	Lucy M.C., Boyd C.K.;
RT	"Bovine somatotropin receptor 1B mRNA.";
RL	Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF044258; AAC02534.1; -.
DR	HSSP; P10912; 1A22.
DR	InterPro; IPR002956; CRLA.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR003528; Hematopo_receptor_L_F1.
DR	Pfam; PF00041; Fn3; 1.
DR	SMART; SM00606; FN3; 1.
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW	Signal; Receptor.
FT	SIGNAL 1 POTENTIAL.
FT	CHAIN 19 634 SOMATOTROPIN RECEPTOR 1B.
FT	SEQUENCE 634 AA; 70914 MW; 176936D32EATC4C9 CRC64;
Query Match	8.88; Score 112.5; DB 6; Length 634;

Best Local Similarity 26.3%; Pred. No. 0.14;
 Matches 35; Conservative 25; Mismatches 60; Indels 13; Gaps 5;

Qy 14 PEEELCFTEREDLVOFFEEAASAGV-GPGNFS-FSFOLEDEPWKLCLRHLQAPTARGAIR 71
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 51 PKFTKRSPELETFESCHWTQANHSIQSOSQVOMFYIRRDIGEWKSC----PDVVSAGE 105

Qy 72 FWCSLPTADNSSFVPLRLRITAASGAPRFHRVTHINEVLLDAPVGLVARLADES---- 126
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 106 NSCFNNSYTSWTPCILKTSNGGIVD-HKCFSEVEDIVQPDPPGNGLNWTLNISLIEH 164

Qy 127 GHWVIVWLPPET 139
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 165 ADILVKWEPPTNT 177

RESULT 15
 Q90WG7 PRELIMINARY; PRT; 626 AA.
 ID Q90WG7;
 AC 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR.
 OS Cynops pyrhogaster (Japanese common newt).
 OC Bukayota; Metacca; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Yamamoto T., Nakayama Y., Matsuda Y., Abe S.-I.;
 RT "Cloning and expression of a cDNA encoding a prolactin receptor of the
 RL Japanese red-bellied newt, *Cynops pyrhogaster*."
 DR EMBL; AB005045; BAB61107.1; -.
 KW SIGNAL; Receptor;
 FT SIGNAL 1
 SEQUENCE 626 AA; 26 POTENTIAL
 SQ B6050DD9C9F58DBE5 CRC64;

Query Match 8.7%; Score 11.5; DB 13; Length 626;
 Best Local Similarity 19.3%; Pred. No. 0.17;
 Matches 40; Conservative 42; Mismatches 88; Indels 37; Gaps 8;

Qy 14 PEEELCFTEREDLVOFFEEAASAGV-GPGNFS-FSFOLEDEPWKLCLRHLQAPTARGAIR 73
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 34 PWNIMCRSPERKETFSQWQPOGSDGGI-PTNNSLLYKTEGKN---TYSECDPYKUSGPNS 88

Qy 74 CSLPTADTSFVPLEL----RITAASGAPRFHRVTHINEVLLDAPVGLVARLADES 127
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 89 CFPDKKHTSITWMMYNTIVNATNEGLSTSDPKF--VDVAVTIVQLRPPNLTSLIYEP 145

Qy 128 HWVIRLPPETPMTS---HTRFELDISAGNG-----AGSVQRVELLEGRTCECVLNL 177
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 146 HILWKWSPPSBADVKSGWVIEYEVQFKSKAKEWETLTAGKQRLKV-----SL 196

Qy 178 RGRTRITIAVARRMAEPSEGFWSAVS 204

Db 197 NPSENNTIVQVCK---SDHGFWSMWS 219

Search completed: August 28, 2002, 17:40:16
 Job time: 547 sec

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